OIPE JCG
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PATENT & TRADEMARK OFFICE

SEQUENCE LISTING

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<110>  BULLERDIEK, Jorn
       RIPPE, Volkhard
       BELGE, Gazanfer
       MEIBOOM, Maren

<120>  Nucleic acid sequences of hyperplasies and tumors of the thyroid

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Thr Arg Ser Arg Arg Arg Lys     Leu Arg     Ile Leu Tyr Pro Lys
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Gln Asn Pro Gln His Val Phe Leu Lys Arg Pro Ala Leu Arg Arg Val
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Cys Gly Ala Leu Ser Ala Pro Ser Pro Pro Arg Asp Gly Ala Ala Ser
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Ser Met Asp Val Pro Phe Cys Leu Leu Ser Cys Cys Pro Cys Tyr Ala
            95                  100                 105

tgg tat tgg ccc att ggc cca aac gcc tgt tct ctg gag agc tga tct         384
Trp Tyr Trp Pro Ile Gly Pro Asn Ala Cys Ser Leu Glu Ser     Ser
        110                 115                 120

aca tcg cag cgg ctg tgt tgc tgc tgg tgc tca ttg tgg gat tca ctt         432
Thr Ser Gln Arg Leu Cys Cys Cys Trp Cys Ser Leu Trp Asp Ser Leu
        125                 130                 135

tca ccg tct gga gac agc ccc aga gca aca ctc ctc ttt act tca ag  g       480
Ser Pro Ser Gly Asp Ser Pro Arg Ala Thr Leu Leu Phe Thr Ser Arg
    140                 145                 150

tcc ccc tgt tgc ctg ttc tcc tct ggt cag cat ctc tgc aca tgt tta         528
Ser Pro Cys Cys Leu Phe Ser Ser Gly Gln His Leu Cys Thr Cys Leu
155                 160                 165                 170

cct gat gat gca gat gac cac tga gac ctg ggc cca atg tgg agt ctg         576
Pro Asp Asp Ala Asp Asp His     Asp Leu Gly Pro Met Trp Ser Leu
                175                 180                 185

gat gtt gat tg  g att tgc tat gta ttt tgg ata tgg gat ccc aca cag       624
Asp Val Asp Trp   Ile Cys Tyr Val Phe Trp Ile Trp Asp Pro Thr Gln
                  190                 195                 200

ctt gga gaa caa tca aca gcc acc agc gtc aag ctc cca aac tcc tca         672
Leu Gly Glu Gln Ser Thr Ala Thr Ser Val Lys Leu Pro Asn Ser Ser
            205                 210                 215

tga aaa cat ccc tag tcc ctt gct gaa tta gtt taa cca cgg aaa agg         720
    Lys His Pro     Ser Leu Ala Glu Leu Val     Pro Arg Lys Arg
            220                     225                 230
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gat ggt cca gtc cac tgg agg tgt cct ctg gat gaa ggg aaa gtg tga        768
Asp Gly Pro Val His Trp Arg Cys Pro Leu Asp Glu Gly Lys Val
                235                 240                 245

agc tct gtg gag cat gaa ggt ggg ata cac tta aag ccc ctt gtg cat        816
Ser Ser Val Glu His Glu Gly Gly Ile His Leu Lys Pro Leu Val His
                250                 255                 260

tgc cag tga gca aac act ttt taa aaa act tta ttt tgt tgt ttg ttt        864
Cys Gln     Ala Asn Thr Phe     Lys Thr Leu Phe Cys Cys Leu Phe
                265                     270                 275

gtt tgt ttg ttt gtt tgt ttg tta tag agg tga gga ctt gct ctg ttg        912
Val Cys Leu Phe Val Cys Leu Leu     Arg     Gly Leu Ala Leu Leu
                280                         285

ccc agg cgg aac ttg aac tcc tgg gct caa gtg atc ctc ctg cct cag        960
Pro Arg Arg Asn Leu Asn Ser Trp Ala Gln Val Ile Leu Leu Pro Gln
290                 295                 300                 305

tct tcc aag cag ctg gga cta cag gta ccc cat cat acc cag ctt aac       1008
Ser Ser Lys Gln Leu Gly Leu Gln Val Pro His His Thr Gln Leu Asn
                310                 315                 320

aaa ata tct tta ttt gat ttg att ttt ttt ctt ttt gag aca gag tct       1056
Lys Ile Ser Leu Phe Asp Leu Ile Phe Phe Leu Phe Glu Thr Glu Ser
            325                 330                 335

cgc tct att gcc cag tct gga gtg cag tgg cat gat ctt ggc tca ctg       1104
Arg Ser Ile Ala Gln Ser Gly Val Gln Trp His Asp Leu Gly Ser Leu
        340                 345                 350

caa cct ccg cct ccc ggg ttc aag tga ttc ccc tgy gtg agc ctc cag       1152
Gln Pro Pro Pro Pro Gly Phe Lys     Phe Pro Cys Val Ser Leu Gln
    355                 360                     365

agt agc tgg aat tac agg cac atg aca ctg tgc cca gct aat ttt tct       1200
Ser Ser Trp Asn Tyr Arg His Met Thr Leu Cys Pro Ala Asn Phe Ser
    370                 375                 380

tta tta gya gag acc agg ttt cac cat gtt ggc cag gct ggt ctt gaa       1248
Leu Leu Xaa Glu Thr Arg Phe His His Val Gly Gln Ala Gly Leu Glu
385                 390                 395                 400

ctc ctg acc tca agt gat cca cct gcc tcg gcc tcc caa agt gct gag       1296
Leu Leu Thr Ser Ser Asp Pro Pro Ala Ser Ala Ser Gln Ser Ala Glu
                405                 410                 415

att aca ggc ctg agc cac cgt gcc cag cca aaa taa ctt taa aaa ctt       1344
Ile Thr Gly Leu Ser His Arg Ala Gln Pro Lys     Leu     Lys Leu
            420                 425                             430

aca ttt tta aaa att gac aaa yaa aag ttg tct atg ttt atg gtg tac       1392
Thr Phe Leu Lys Ile Asp Lys Xaa Lys Leu Ser Met Phe Met Val Tyr
                435                 440                 445

aat tgc ata tat tat atg tat taa aat tgt gta tgt tta tgg tat           1437
Asn Cys Ile Tyr Tyr Met Tyr     Asn Cys Val Cys Leu Trp Tyr
            450                     455                 460


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tgatgttgga tgaacaggga cctgggttaa tcttgcccta ctctctctaa ttcaggtacc     120

agccagacga gaatttcagc aagaacgaga agccgaagga ggaagtagtt gagatgaatt     180

ctgtacccaa agcagaatcc ccagcatgtg ttcctgaagc gtccagcact ccggcgagtc     240

tgtggagccc tgtcagcacc atccccaccc cgagatgggg ccgcatcgtc tatggatgtg     300

cctttctgct tgttgtcctg ctgtccatgc tatgcctggt attggcccat tggcccaaac     360

gcctgttctc tggagagctg atctacatcg cagcggctgt gttgctgctg gtgctcattg     420

tgggattcac tttcaccgtc tggagacagc cccagagcaa cactcctctt tacttcaagg     480

tcccccctgtt gcctgttctc ctctggtcag catctctgca catgtttacc tgatgatgca     540

gatgaccact gagacctggg cccaatgtgg agtctggatg ttgattggat ttgctatgta     600

ttttggatat gggatcccac acagcttgga gaacaatcaa cagccaccag cgtcaagctc     660

ccaaactcct catgaaaaca tccctagtcc cttgctgaat tagtttaacc acggaaaagg     720

gatggtccag tccactggag gtgtcctctg gatgaaggga aagtgtgaag ctctgtggag     780

catgaagaga tggagtttca ccttgttgcc gaggctggtc ttgaactcct gagctgaagc     840

catcctcctg cctctggcct ctaaaagtgc tgggattcca ggcgtgagcc agcgtgcccg     900

gccatcatgt ttacttcaaa cagattttct ctggcgtctt ctaggacact tgtatctgat     960

ctttactgaa agtcacattc ttagcaagac ttaaccttac atcctgagta aaattgcgaa    1020

ttccacagat gccctcaatc tttcctgacc tcggctcctc ttctgtttcc cggcatggct    1080

tgaagcgcaa cggcattcta cctgtttact caggatgtgt cttaccatta aagtccctgc    1140

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Trp Ile Trp Val Asp Glu Thr Ser Asp Thr Trp Glu Leu Pro Trp Val
1               5                   10                  15

tat tag gct ctc tga tgt tgg atg aac agg gac ctg ggt taa tct tgc       96
Tyr     Ala Leu     Cys Trp Met Asn Arg Asp Leu Gly     Ser Cys
                    20                  25

cct act ctc tct aat tca ggt acc agc cag acg aga att tca gca aga      144
Pro Thr Leu Ser Asn Ser Gly Thr Ser Gln Thr Arg Ile Ser Ala Arg
30                  35                  40                  45

acg aga agc cga agg agg aag tag ttg aga tga att ctg tac cca aag      192
Thr Arg Ser Arg Arg Arg Lys     Leu Arg     Ile Leu Tyr Pro Lys
                50                          55

cag aat ccc cag cat gtg ttc ctg aag cgt cca gca ctc cgg cga gtc      240
Gln Asn Pro Gln His Val Phe Leu Lys Arg Pro Ala Leu Arg Arg Val
60                  65                  70                  75

tgt gga gcc ctg tca gca cca tcc cca ccc cga gat ggg gcc gca tcg      288
Cys Gly Ala Leu Ser Ala Pro Ser Pro Pro Arg Asp Gly Ala Ala Ser
                80                  85                  90

tct atg gat gtg cct ttc tgc ttg gtgagcagtg gcgtttctcc gcggggtgtt      342
Ser Met Asp Val Pro Phe Cys Leu
            95

ttgaacctga tagcatgcgg caggggggccg agtagggagt gtggggcttt ggtagttgag      402

aggagttgtg aagatgtggt ggcccttctt agtaggcgca cttttggccg ggcacagtgg      462

attacacatg gaatcccagc actttgggag gctgaggcgg gacaactgct tgagcctggg      522

cagtcgaggc ttcagtgaat caagaccaca ccactgcact gtagtctggg caatggggcg      582

agatcccatc tcaaaaaaca aacaaaaagc catatatata tatacacaca cacacacata      642

tatacacaca cacacacata catatacaca cacaaatata tatatataaa attaaaagtt      702

taggctgggt gtggtggctc actttagaag gctgaggcaa gtggatcact tgaggtgagg      762

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aggtcaggca cagtggctca cgcctgtaat cccagcactc tgggaggccg ggtgccgggg      882

gggagtggat cacaaggtca ggagttcgag atcagcctgg ccaacatggt gaaaccccat      942

ctctactaaa aatacaaaaa ttagccgagc acggtggcag acgcctgtaa tcccagctac     1002

tcggggagac tgaggcagga gaattatttg aaccggagag gccgagtttc cagtgagcca     1062

agatcacgcc actgcacttc agcctgggca acagagaaag actttttctc aaaaaaaaaa     1122

aaaaaataca aaaaattagc tgggtgtggt ggcagttacc tgtaatccca gctacttggg     1182
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aggctgaggc aggagaatca cttgaaccca ggaggcagag gttgcagtga gccaagattg    1242

tgccactgca ctccatcctg ggcaacaaga gtgaaactgc atctcaaaaa aaaaaaaaaa    1302

gtatttgggt gtgctgacac gtgcctgtag tccctacttg ggaggctggc acacacacac    1362

acacacacac acacacacac acacacacac acacccatac ccatatatat ggtttggggg    1422

ataggatgtg gcccgagatc ttcacttatt tagcttctga agttgaacct gttctcccca    1482

accttgaccc ttttccag ttg tcc tgc tgt cca tgc tat gcc tgg tat tgg      1533
                    Leu Ser Cys Cys Pro Cys Tyr Ala Trp Tyr Trp
                    100                 105                 110

ccc att ggc cca aac gcc tgt tct ctg gag agc tga tct aca tcg cag      1581
Pro Ile Gly Pro Asn Ala Cys Ser Leu Glu Ser     Ser Thr Ser Gln
                115                 120                     125

cgg ctg tgt tgc tgc tgg tgc tca ttg tgg gat tca ctt tca ccg tct      1629
Arg Leu Cys Cys Cys Trp Cys Ser Leu Trp Asp Ser Leu Ser Pro Ser
                130                 135                 140

gga gac agc ccc aga gca aca ctc ctc ttt act tca ag  gtaggtggcc      1677
Gly Asp Ser Pro Arg Ala Thr Leu Leu Phe Thr Ser Arg
            145                 150

ttatgtcccc acaccaccct cctgagtcag tggactctgc atgcctcaag ctctaaatac    1737

tctacgggac caggggtaaa aagggcagtt gcgaaaaacc aatggactgt tcatggacac    1797

cccctccagc ccccacatat cagtacttcc caaaacctgt ctcttccaga acacccaatg    1857

gaatacctac tcagaacagg cattgagcca ggtgaggtgg ctcacacctg taatcccagc    1917

actttgggag gccaaggcgg gtggatcact tgaggcgagg agttcgggac cagcctgacc    1977

aacatggtga aattccggtt ctactaaaaa tacaaaaatt agccgggcat ggtggtgtgt    2037

gccggtaatc ccagctactc aggaggctga ggcaggagaa tcgcttgaac ccaggaggcg    2097

gatgttgcat tcagctgaga tcgcgccact gcactccagc ctgggtgaca cagcaagact    2157

ctgtctcaaa aaaaaaaaaa aaagaatagg cattgaatat gcgactgcaa cagagctgag    2217

gccttcccac cccttggaat aagggtccct tgcagacgtt cgtggtgtgc tcacggttaa    2277

cgctttgcct gcag g tcc ccc tgt tgc ctg ttc tcc tct ggt cag cat ctc    2328
                  Ser Pro Cys Cys Leu Phe Ser Ser Gly Gln His Leu
                  155                 160                 165

tgc aca tgt tta cct gat gat gca gat gac cac tga gac ctg ggc cca      2376
Cys Thr Cys Leu Pro Asp Asp Ala Asp Asp His     Asp Leu Gly Pro
            170                 175                     180

atg tgg agt ctg gat gtt gat tg  gtgagtggct tcctggaaaa aaagaggcct    2429
Met Trp Ser Leu Asp Val Asp Trp
            185

cttgggtgtc tgagcccaac actcttcctg cgacctttcc ctatagctgt ctcaggctaa    2489

cagtgtgggg tgtgcctgta gtcccagcta ctcaggagat gaaggcagga gcatcgcttg    2549

agaccaggag ctccagacca gcctgggcaa catggcgaga ctccacctct accaaaataa    2609

aaaactggcc gcacgcagtg gctcgcacct ataatcccag cacttcaggg ggccaaggca    2669

ggtgggtcac ctaagatcag gagctcaaga acagcctggc caacatggtg aaaccccatc    2729

tctactaaaa atacaaaaaa gtagccgggc gtggtggcgg gcgcctgtaa tcccacctac    2789
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tcaggaggct gaggcatgag aattgcttga acccaggagg cagagtttgc ggtgagccga    2849

gatcatgcca ttgcactcca gcgcaggcga caggagctga gattgtgcca ctgcactcca    2909

gcctgggtga cagagtgaga tgctgtctca aaaaaaaaaa aaaaaaaaaa aaaaaattag    2969

ccaggcacgg tggcacctgc ctgtagtcac atctattctg aaggctgagg tgggaggatc    3029

gcttgaaccc aggaggtcga ggctgcagtg agccatgatc atgccactgc actccagcct    3089

gggcaatgga gcgaagctct atttctaaat aaaagaaaca agaaaacctc caaataaaca    3149

aaccacagta taatcgctat agggcattta taagggaagg ggtgactaca tttcctttca    3209

ttgtctcatt tccctgctag g att tgc tat gta ttt tgg ata tgg gat ccc      3260
                        Ile Cys Tyr Val Phe Trp Ile Trp Asp Pro
                        190                 195

aca cag ctt gga gaa caa tca aca gcc acc agc gtc aag ctc cca aac      3308
Thr Gln Leu Gly Glu Gln Ser Thr Ala Thr Ser Val Lys Leu Pro Asn
200                 205                 210                 215

tcc tca tga aaa cat ccc tag tcc ctt gct gaa tta gtt taa cca cgg      3356
Ser Ser     Lys His Pro     Ser Leu Ala Glu Leu Val     Pro Arg
                    220                     225

aaa agg gat ggt cca gtc cac tgg agg tgt cct ctg gat gaa ggg aaa      3404
Lys Arg Asp Gly Pro Val His Trp Arg Cys Pro Leu Asp Glu Gly Lys
    230                 235                 240

gtg tga agc tct gtg gag cat gaa ggt ggg ata cac tta aag ccc ctt      3452
Val     Ser Ser Val Glu His Glu Gly Gly Ile His Leu Lys Pro Leu
245                     250                 255

gtg cat tgc cag tga gca aac act ttt taa aaa act tta ttt tgt tgt      3500
Val His Cys Gln     Ala Asn Thr Phe     Lys Thr Leu Phe Cys Cys
260                     265                     270

ttg ttt gtt tgt ttg ttt gtt tgt ttg tta tag agg tga gga ctt gct      3548
Leu Phe Val Cys Leu Phe Val Cys Leu Leu     Arg     Gly Leu Ala
    275                 280                         285

ctg ttg ccc agg cgg aac ttg aac tcc tgg gct caa gtg atc ctc ctg      3596
Leu Leu Pro Arg Arg Asn Leu Asn Ser Trp Ala Gln Val Ile Leu Leu
        290                 295                 300

cct cag tct tcc aag cag ctg gga cta cag gta ccc cat cat acc cag      3644
Pro Gln Ser Ser Lys Gln Leu Gly Leu Gln Val Pro His His Thr Gln
    305                 310                 315

ctt aac aaa ata tct tta ttt gat ttg att ttt ttt ctt ttt gag aca      3692
Leu Asn Lys Ile Ser Leu Phe Asp Leu Ile Phe Phe Leu Phe Glu Thr
320                 325                 330                 335

gag tct cgc tct att gcc cag tct gga gtg cag tgg cat gat ctt ggc      3740
Glu Ser Arg Ser Ile Ala Gln Ser Gly Val Gln Trp His Asp Leu Gly
                340                 345                 350

tca ctg caa cct ccg cct ccc ggg ttc aag tga ttc ccc tgy gtg agc      3788
Ser Leu Gln Pro Pro Pro Pro Gly Phe Lys     Phe Pro Cys Val Ser
            355                 360                     365

ctc cag agt agc tgg aat tac agg cac atg aca ctg tgc cca gct aat      3836
Leu Gln Ser Ser Trp Asn Tyr Arg His Met Thr Leu Cys Pro Ala Asn
            370                 375                 380

ttt tct tta tta gya gag acc agg ttt cac cat gtt ggc cag gct ggt      3884
Phe Ser Leu Leu Xaa Glu Thr Arg Phe His His Val Gly Gln Ala Gly
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        385                 390                 395

ctt gaa ctc ctg acc tca agt gat cca cct gcc tcg gcc tcc caa agt      3932
Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Ala Ser Ala Ser Gln Ser
    400                 405                 410

gct gag att aca ggc ctg agc cac cgt gcc cag cca aaa taa ctt taa      3980
Ala Glu Ile Thr Gly Leu Ser His Arg Ala Gln Pro Lys     Leu
415                 420                 425

aaa ctt aca ttt tta aaa att gac aaa yaa aag ttg tct atg ttt atg      4028
Lys Leu Thr Phe Leu Lys Ile Asp Lys Xaa Lys Leu Ser Met Phe Met
    430                 435                 440

gtg tac aat tgc ata tat tat atg tat taa aat tgt gta tgt tta tgg      4076
Val Tyr Asn Cys Ile Tyr Tyr Met Tyr     Asn Cys Val Cys Leu Trp
445                 450                 455

tat acatgaagct tggaaatatg tatacattgt ggaattgcta aatcaggttg           4129
Tyr
460

attaacgtat tcattacctt acataccttt tttttttttg agatggagtc tccctctgtc    4189

gcccagactg gagtgcagta gtgtgatctc agctcactgc aacctccgcc tcccaggttc    4249

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ccggctaatt tttgtgtttt tagtagagac ggggtttcac catgtcggtc aggctggtct    4369

cgaatgcctg acctcatgat ctgcccgcct cggcctccca aagtgctggg attacaggcg    4429

tgagccacca cacccagcct tacgtgccat tttttttttt ttttgtggta aaaacattta    4489

aaatggccgg gtgcggtggc tcatgcctgt aatcccagca ctttgggagg ccaaggcagg    4549

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tactaaaaat acaaaaaatt agctggggcg cagtggcagg tgcctgtaat cccagctact    4669

cgggagactg aggcttgaac ccagaggcag aggttgcagt gagctgagat tgcaccattg    4729

cactccagct tgggcaacaa gagtgaaatt catctcaaaa aaaaaaaaaa atagccaggt    4789

gcggtctgga actcccggcc tcaagtgatc ctcttgcctc agcctcccga gtagctggga    4849

atacaggcat gcgctaccac accagggtaa tttttgtatt tacagtag aga tgg agt     4906
                                                     Arg Trp Ser


ttc acc ttg ttg ccg agg ctg gtc ttg aac tcc tga gct gaa gcc atc      4954
Phe Thr Leu Leu Pro Arg Leu Val Leu Asn Ser     Ala Glu Ala Ile
    465                 470                     475

ctc ctg cct ctg gcc tct aaa agt gct ggg att cca ggc gtg agc cag      5002
Leu Leu Pro Leu Ala Ser Lys Ser Ala Gly Ile Pro Gly Val Ser Gln
    480                 485                     490

cgt gcc cgg cca tca tgt tta ctt caa aca gat ttt ctc tgg cgt ctt      5050
Arg Ala Arg Pro Ser Cys Leu Leu Gln Thr Asp Phe Leu Trp Arg Leu
495                 500                 505                 510

cta gga cac ttg tat ctg atc ttt act gaa agt cac att ctt agc aag      5098
Leu Gly His Leu Tyr Leu Ile Phe Thr Glu Ser His Ile Leu Ser Lys
                515                 520                 525

act taa cct tac atc ctg agt aaa att gcg aat tcc aca gat gcc ctc      5146
Thr     Pro Tyr Ile Leu Ser Lys Ile Ala Asn Ser Thr Asp Ala Leu
                530                 535                 540
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aat ctt tcc tga cct cgg ctc ctc ttc tgt ttc ccg gca tgg ctt gaa          5194
Asn Leu Ser     Pro Arg Leu Leu Phe Cys Phe Pro Ala Trp Leu Glu
                545                 550                 555

gcg caa cgg cat tct acc tgt tta ctc agg atg tgt ctt acc att aaa          5242
Ala Gln Arg His Ser Thr Cys Leu Leu Arg Met Cys Leu Thr Ile Lys
            560                     565             570

gtc cct gcc tgc aga gca gtt ggc ttg att tca cct                          5278
Val Pro Ala Cys Arg Ala Val Gly Leu Ile Ser Pro
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<212>  PRT
<213>  Homo sapiens


<220>
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<223>  protein sequence of ORF 1 of mRNA of CAT-A

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Met Gly Pro His Arg Leu Trp Met Cys Leu Ser Ala Cys Cys Pro Ala
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Val His Ala Met Pro Gly Ile Gly Pro Leu Ala Gln Thr Pro Val Leu
            20                  25                  30


Trp Arg Ala Asp Leu His Arg Ser Gly Cys Val Ala Ala Gly Ala His
        35                  40                  45


Cys Gly Ile His Phe His Arg Leu Glu Thr Ala Pro Glu Gln His Ser
    50                  55                  60


Ser Leu Leu Gln Gly Pro Pro Val Ala Cys Ser Pro Leu Val Ser Ile
65                  70                  75                  80


Ser Ala His Val Tyr Leu Met Met Gln Met Thr Thr Glu Thr Trp Ala
                85                  90                  95


Gln Cys Gly Val Trp Met Leu Ile Gly Phe Ala Met Tyr Phe Gly Tyr
            100                 105                 110


Gly Ile Pro His Ser Leu Glu Asn Asn Gln Gln Pro Pro Ala Ser Ser
        115                 120                 125


Ser Gln Thr Pro His Glu Asn Ile Pro Ser Pro Leu Leu Asn
    130                 135                 140


<210>  14
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<220>
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<223>  protein sequence of ORF 2 of mRNA of CAT-A

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Met Asn Ser Val Pro Lys Ala Glu Ser Pro Ala Cys Val Pro Glu Ala
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Ser Ser Thr Pro Ala Ser Leu Trp Ser Pro Val Ser Thr Ile Pro Thr
            20                  25                  30

Pro Arg Trp Gly Arg Ile Val Tyr Gly Cys Ala Phe Leu Leu Val Val
        35                  40                  45

Leu Leu Ser Met Leu Cys Leu Val Leu Ala His Trp Pro Lys Arg Leu
    50                  55                  60

Phe Ser Gly Glu Leu Ile Tyr Ile Ala Ala Ala Val Leu Leu Leu Val
65                  70                  75                  80

Leu Ile Val Gly Phe Thr Phe Thr Val Trp Arg Gln Pro Gln Ser Asn
                85                  90                  95

Thr Pro Leu Tyr Phe Lys Val Pro Leu Leu Pro Val Leu Leu Trp Ser
            100                 105                 110

Ala Ser Leu His Met Phe Thr
        115


<210>  15
<211>  140
<212>  PRT
<213>  Homo sapiens


<220>
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<223>  protein sequence of ORF 3 of mRNA of CAT-A

<400>  15

Phe Arg Tyr Gln Pro Asp Glu Asn Phe Ser Lys Asn Glu Lys Pro Lys
1               5                   10                  15

Glu Glu Val Val Glu Met Asn Ser Val Pro Lys Ala Glu Ser Pro Ala
            20                  25                  30

Cys Val Pro Glu Ala Ser Ser Thr Pro Ala Ser Leu Trp Ser Pro Val
        35                  40                  45

Ser Thr Ile Pro Thr Pro Arg Trp Gly Arg Ile Val Tyr Gly Cys Ala
    50                  55                  60

Phe Leu Leu Val Val Leu Leu Ser Met Leu Cys Leu Val Leu Ala His
65                  70                  75                  80
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Trp Pro Lys Arg Leu Phe Ser Gly Glu Leu Ile Tyr Ile Ala Ala Ala
                85                  90                  95


Val Leu Leu Leu Val Leu Ile Val Gly Phe Thr Phe Thr Val Trp Arg
            100                 105                 110


Gln Pro Gln Ser Asn Thr Pro Leu Tyr Phe Lys Val Pro Leu Leu Pro
        115                 120                 125


Val Leu Leu Trp Ser Ala Ser Leu His Met Phe Thr
    130                 135                 140


<210>  16
<211>  1686
<212>  DNA
<213>  Homo sapiens


<220>
<221>  misc_feature
<223>  Genomic sequence of the DC2 homologous gene

<220>
<221>  exon
<222>  (1)..(288)
<223>  Exon 3 of the homologous gene to DC2

<220>
<221>  misc_feature
<222>  (1)..(288)
<223>  Complementary (1..288) homologous to XM_034710-mRNA end section
       nucleotide 782..1070 ( XM_034710: mRNA of homo sapiens DC2)

<220>
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<222>  (621)..(863)
<223>  Exon 2 of the homologous gene to DC2

<220>
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<222>  (621)..(863)
<223>  Complementary (621..863) homologous to XM_034710-mRNA section
       nucleotide 539..782 ( XM_034710: mRNA of homo sapiens DC2)

<220>
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<222>  (1183)..(1686)
<223>  Exon 1 of the homologous gene to DC2

<220>
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<222>  (1183)..(1686)
<223>  Complementary (1183..1686) homologous to XM_034710 mRNA section
       nucleotide 1183..1686 (XM_034710: mRNA of homo sapiens DC2)

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ttt ttt aat tag tat tta ttt ctg ttc ctt tca tac atg tta ttg ttc       48
Phe Phe Asn     Tyr Leu Phe Leu Phe Leu Ser Tyr Met Leu Leu Phe
1                   5                   10                  15

agg cag cag tct tac ata cct atc tga aat aat cta cca tca cac act       96
Arg Gln Gln Ser Tyr Ile Pro Ile     Asn Asn Leu Pro Ser His Thr
                20                      25                  30

cta gtt aaa gcc aaa gct ccg tag gta aag ctg acc agc tgt cca gag      144
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```
Leu Val Lys Ala Lys Ala Pro     Val Lys Leu Thr Ser Cys Pro Glu
                35                      40                  45

ttc tca gct cat gga atc ttg ctt ctt gat ttt atg tta att tct gaa      192
Phe Ser Ala His Gly Ile Leu Leu Leu Asp Phe Met Leu Ile Ser Glu
                50                  55                  60

agt cag aaa tgt cat ctc caa aaa gtg tta agg ggg ttg taa aaa ata      240
Ser Gln Lys Cys His Leu Gln Lys Val Leu Arg Gly Leu     Lys Ile
            65                  70                      75

atc act ata ttt gct att ata gtt gta ggt atg cag tat att ttc ttt      288
Ile Thr Ile Phe Ala Ile Ile Val Val Gly Met Gln Tyr Ile Phe Phe
            80                  85                  90

tctttctttc tttctttttt tttttttgaa acagagtctc gctctgtcgc ccaggctgga    348

gtgcagtggc agcgatctag gctcactgca gcctccgcct cccaggttca cgtgattctc    408

ctgcctcagc cttccaagta gctgggatta caggtgcccc gccaccacca cgcccggcta    468

atttttgtat ttttagtaga gatggggttt caacatggtg gccaggctgg tctggaactc    528

ctgacctcgt gatctgccca ccttggcctc ccaaagtgct gggactacag aagtgagcca    588

ccgcgcctgg cttgtatttt cttaaagaaa ta aaa aac taa gaa gaa aat gcc      641
                                    Lys Asn     Glu Glu Asn Ala
                                                95

act cat cat cat tgg tat agc aat gtg gtc agc agg aaa aga aaa tac      689
Thr His His His Trp Tyr Ser Asn Val Val Ser Arg Lys Arg Lys Tyr
    100                 105                 110

tgt gat aaa ttt gtc tct tta ata aag aag aaa ttc tag tcc aag ctt      737
Cys Asp Lys Phe Val Ser Leu Ile Lys Lys Lys Phe     Ser Lys Leu
115                 120                 125

caa tac act tcc tgg ttt ttc act aga tat ttc ttt tac tgc tgc tct      785
Gln Tyr Thr Ser Trp Phe Phe Thr Arg Tyr Phe Phe Tyr Cys Cys Ser
130                 135                 140                 145

tcc ttc ttt tct aca tct cat att aga gga ttg gac agc ctt taa aac      833
Ser Phe Phe Ser Thr Ser His Ile Arg Gly Leu Asp Ser Leu     Asn
                150                 155                     160

ttc att gac agg agc aaa tcc agt atg cac tgatttcttt ttttttttct        883
Phe Ile Asp Arg Ser Lys Ser Ser Met His
                165                 170

tttttttttt tttggtgaga cggagattta ctcttgttgt ccaggctgga gtgcaatggt    943

gcgatctcgg ctcaccgcat cctctgcctc ccgggttcaa gcaattctcc tgcctcagcc   1003

tcccgagtag ctgggattac agacatgtgt caccacgcct ggctaatttt gtatttgtag   1063

tagggatggg gttttaccat gttgcccagg ctgatctcga actcctgacc tcagataatc   1123

cgctcgcctc ggcctcccaa agtgctggga ttgacaggcg tgagccactg cacccagcc    1182

tga ttt ctt ctt aaa ggc act cta acc cat cag aga gcc cgg tag ttt     1230
    Phe Leu Leu Lys Gly Thr Leu Thr His Gln Arg Ala Arg     Phe
                    175                 180

cat tct cac gaa tac tct agc cgt gaa aaa aac tca ata gga cac aga     1278
His Ser His Glu Tyr Ser Ser Arg Glu Lys Asn Ser Ile Gly His Arg
185                 190                 195                 200

cga atc caa cga ata gaa gaa gaa atc tat tga gtt ttg gga tat ttg     1326
Arg Ile Gln Arg Ile Glu Glu Glu Ile Tyr     Val Leu Gly Tyr Leu
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                205                 210                     215

gtg cat tcg atc ggt cca gga tta tga aac cta aac ctc cca ttg taa       1374
Val His Ser Ile Gly Pro Gly Leu     Asn Leu Asn Leu Pro Leu
                220                     225

aca gga agc tgg atc caa gtc ctt cca taa taa tat tgt cca ctt act       1422
Thr Gly Ser Trp Ile Gln Val Leu Pro         Tyr Cys Pro Leu Thr
230                 235                         240

ctg tag gcc aag aaa gct act ggc ctc tga tgc cct tgt tca tca gtc       1470
Leu     Ala Lys Lys Ala Thr Gly Leu     Cys Pro Cys Ser Ser Val
        245                 250                     255

ata gag cca aca cct ggc ggt tca acc gta aca tca taa acg att cct       1518
Ile Glu Pro Thr Pro Gly Gly Ser Thr Val Thr Ser     Thr Ile Pro
        260                 265                     270

ctg gtg atg agg aag taa gac acc acc acc aga gca tac ata gtc atg       1566
Leu Val Met Arg Lys     Asp Thr Thr Thr Arg Ala Tyr Ile Val Met
        275                     280                 285

gcc aac ggc atg tgc agc cag ggc ggc ttc ttc agc ttc agg ttg gga       1614
Ala Asn Gly Met Cys Ser Gln Gly Gly Phe Phe Ser Phe Arg Leu Gly
        290                 295                 300

cat tca agc gct aag aac ggg aca cgg tac aaa gtc tcc atg ttg gtg       1662
His Ser Ser Ala Lys Asn Gly Thr Arg Tyr Lys Val Ser Met Leu Val
    305                 310                 315

gca gca agg gcc att ctc ggc ctc                                       1686
Ala Ala Arg Ala Ile Leu Gly Leu
320                 325


<210>  17
<211>  1035
<212>  DNA
<213>  Homo sapiens


<220>
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<223>  Possible mRNA of DC2 homologous gene

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<222>  (1)..(504)
<223>  Exon 1 of homologous gene to DC2

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<223>  Largely homologous to the nucleotides 37-538 of XM_034710 (mRNA
       of DC2)

<220>
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<222>  (504)..(747)
<223>  Largely homologous to the nucleotides 539-782 of XM_034710 (mRNA
       of DC2)

<220>
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<223>  Exon 2 of homologous gene to DC2

<220>
<221>  exon
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<222>  (748)..(1035)
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<223>  Largely homologous to the nucleotides 782-1070 of XM_034710 (mRNA
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gag gcc gag aat ggc cct tgc tgc cac caa cat gga gac ttt gta ccg          48
Glu Ala Glu Asn Gly Pro Cys Cys His Gln His Gly Asp Phe Val Pro
1               5                   10                  15

tgt ccc gtt ctt agc gct tga atg tcc caa cct gaa gct gaa gaa gcc          96
Cys Pro Val Leu Ser Ala     Met Ser Gln Pro Glu Ala Glu Glu Ala
            20                      25                  30

gcc ctg gct gca cat gcc gtt ggc cat gac tat gta tgc tct ggt ggt         144
Ala Leu Ala Ala His Ala Val Gly His Asp Tyr Val Cys Ser Gly Gly
            35                  40                  45

ggt gtc tta ctt cct cat cac cag agg aat cgt tta tga tgt tac ggt         192
Gly Val Leu Leu Pro His His Gln Arg Asn Arg Leu     Cys Tyr Gly
        50                  55                      60

tga acc gcc agg tgt tgg ctc tat gac tga tga aca agg gca tca gag         240
    Thr Ala Arg Cys Trp Leu Tyr Asp         Thr Arg Ala Ser Glu
            65                  70                          75

gcc agt agc ttt ctt ggc cta cag agt aag tgg aca ata tta tta tgg         288
Ala Ser Ser Phe Leu Gly Leu Gln Ser Lys Trp Thr Ile Leu Leu Trp
                80                  85                  90

aag gac ttg gat cca gct tcc tgt tta caa tgg gag gtt tag gtt tca         336
Lys Asp Leu Asp Pro Ala Ser Cys Leu Gln Trp Glu Val     Val Ser
            95                  100                     105

taa tcc tgg acc gat cga atg cac caa ata tcc caa aac tca ata gat         384
    Ser Trp Thr Asp Arg Met His Gln Ile Ser Gln Asn Ser Ile Asp
                110                 115                 120

ttc ttc ttc tat tcg ttg gat tcg tct gtg tcc tat tga gtt ttt ttc         432
Phe Phe Phe Tyr Ser Leu Asp Ser Ser Val Ser Tyr     Val Phe Phe
            125                 130                     135

acg gct aga gta ttc gtg aga atg aaa cta ccg ggc tct ctg atg ggt         480
Thr Ala Arg Val Phe Val Arg Met Lys Leu Pro Gly Ser Leu Met Gly
            140                 145                 150

tag agt gcc ttt aag aag aaa tca gtg cat act gga ttt gct cct gtc         528
    Ser Ala Phe Lys Lys Lys Ser Val His Thr Gly Phe Ala Pro Val
            155                 160                 165

aat gaa gtt tta aag gct gtc caa tcc tct aat atg aga tgt aga aaa         576
Asn Glu Val Leu Lys Ala Val Gln Ser Ser Asn Met Arg Cys Arg Lys
        170                 175                 180

gaa gga aga gca gca gta aaa gaa ata tct agt gaa aaa cca gga agt         624
Glu Gly Arg Ala Ala Val Lys Glu Ile Ser Ser Glu Lys Pro Gly Ser
    185                 190                 195

gta ttg aag ctt gga cta gaa ttt ctt ctt tat taa aga gac aaa ttt         672
Val Leu Lys Leu Gly Leu Glu Phe Leu Leu Tyr     Arg Asp Lys Phe
200                 205                 210

atc aca gta ttt tct ttt cct gct gac cac att gct ata cca atg atg         720
Ile Thr Val Phe Ser Phe Pro Ala Asp His Ile Ala Ile Pro Met Met
215                 220                 225                     230
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atg agt ggc att ttc ttc tta gtt ttt aaa gaa aat ata ctg cat acc       768
Met Ser Gly Ile Phe Phe Leu Val Phe Lys Glu Asn Ile Leu His Thr
                235                 240                 245

tac aac tat aat agc aaa tat agt gat tat ttt tta caa ccc cct taa       816
Tyr Asn Tyr Asn Ser Lys Tyr Ser Asp Tyr Phe Leu Gln Pro Pro
            250                 255                 260

cac ttt ttg gag atg aca ttt ctg act ttc aga aat taa cat aaa atc       864
His Phe Leu Glu Met Thr Phe Leu Thr Phe Arg Asn     His Lys Ile
            265                 270                     275

aag aag caa gat tcc atg agc tga gaa ctc tgg aca gct ggt cag ctt       912
Lys Lys Gln Asp Ser Met Ser     Glu Leu Trp Thr Ala Gly Gln Leu
            280                 285                 290

tac cta cgg agc ttt ggc ttt aac tag agt gtg tga tgg tag att att       960
Tyr Leu Arg Ser Phe Gly Phe Asn     Ser Val     Trp     Ile Ile
            295                     300

tca gat agg tat gta aga ctg ctg cct gaa caa taa cat gta tga aag      1008
Ser Asp Arg Tyr Val Arg Leu Leu Pro Glu Gln     His Val     Lys
305                 310                 315

gaa cag aaa taa ata cta att aaa aaa                                  1035
Glu Gln Lys     Ile Leu Ile Lys Lys
    320                     325
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<210> 18
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<220>
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Gly Ala Pro Gly Val Pro Leu Pro Ala Trp Arg Ala Pro His Leu Glu
1               5                   10                  15

gtg cct tgc ccc tct cct gcc cac ctc gga att tcc ctg tgg ctc ctt        96
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Val Pro Cys Pro Ser Pro Ala His Leu Gly Ile Ser Leu Trp Leu Leu
            20                  25                  30

tga tcc ttc gag tct cca gct cct ctc cct tcc acc tgt ttc ccc caa       144
    Ser Phe Glu Ser Pro Ala Pro Leu Pro Ser Thr Cys Phe Pro Gln
            35                  40                  45

gaa agg cag gat cct ggt ccc tgc tac gtt tct ggg gcc atg gct ggt       192
Glu Arg Gln Asp Pro Gly Pro Cys Tyr Val Ser Gly Ala Met Ala Gly
        50                  55                  60

ctg ggc ccc ggc gta ggc gat tca gag ggg gga ccc cgg ccc ctg ttt       240
Leu Gly Pro Gly Val Gly Asp Ser Glu Gly Gly Pro Arg Pro Leu Phe
    65                  70                  75

tgc aga aag ggg gcc ctg agg cag aag gtg gtc cac gaa gtc aag agc       288
Cys Arg Lys Gly Ala Leu Arg Gln Lys Val Val His Glu Val Lys Ser
80                  85                  90                  95

cac aag ttc acc gct cgc ttc ttc aag cag ccc acc ttc tgc agc cac       336
His Lys Phe Thr Ala Arg Phe Phe Lys Gln Pro Thr Phe Cys Ser His
                100                 105                 110

tgc acc gac ttc atc tgg tga ggg aag ggg gctgggggac tgggggacga         386
Cys Thr Asp Phe Ile Trp     Gly Lys Gly
            115                 120

ggggactagg ggtgcagact cctatcacgc cgacccctgt ggaaggaaga aggagggggc     446

tgtagtcccg actcccaggt tctaggatgg ccagggaacg ctgggagctt cgactcctgg     506

gtttcagtga ggaggaggct ggttcctgga gtgctgggtc cgagggagga ggaggctgga     566

ggacagaggt cctggagtct tgggtctgag ggaggaaggg cctgggggc tgggagcctg      626

gattcctggg tctgaaggag gaagaaactg gggctgaac tccagtctaa gggaagaagg      686

gctgggggcc aaaatttctg ggttctagaa agaggaggtg gccggggctt ggacacctgg     746

gccctgcggg aggagggtca gagagcgcag gccccctgtg gctcgcagag gttgggggtc     806

caggtacccc tttctgcact gacctaggat ccctgactct tccaggggta tcggaaa        863

gca ggg cct gca atg tca agg taa gag ctg ggg accggggctc ctgggacccct    916
Ala Gly Pro Ala Met Ser Arg     Glu Leu Gly
                125                 130

caggagggtg gaggctgggg ccccacagct gaggctgctt gacacacgtg ttctctggtc     976

cccagagagg cgcgggggag cccggggcgg ggggtgtggc agagacacag cctgtggtgg    1036

ggagggagct ttgatggtgg ggccaccgcg gaggtggtgc tgggggcccc tccctcggcc    1096

ggctccaggt ggggacagat atttggagaa tctgttgcca tgggaacatg gagatttgga    1156

aaaggggagc tgaagggggg aagggggagg gggctggaga tgcaaagtca gagccccccc    1216

ccaccccagg ctgccgtcgc catgacaaca ccagccgtcc taggcagggg caggccgggt    1276

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gcgggccggc agcagcgccc ccagactcac ttctgcccaa gttgctgctt cctgggctgc    1456

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ctccgtctgt gtctctatga ttttcatcta tagtctgcag ctttg tgg ttc atc gac   1873
                                                  Trp Phe Ile Asp


gat gcc acg aat ttg tga cct tcg agt gtc cag gcg ctg gga agg gcc     1921
Asp Ala Thr Asn Leu     Pro Ser Ser Val Gln Ala Leu Gly Arg Ala
135                     140                 145

ccc aga cgg acg tga gtg ctc gga cacctggttc tcctcctcgg gccgtgcccc    1975
Pro Arg Arg Thr     Val Leu Gly
150                     155

cgccctcacc ccctcggcgt ccgtcccaat ttctcctgct atttttatgg ctgggagggg   2035

agggggggctg gagagatagg gggagctatc tggcccagat tccttgccct tggcctggaa   2095

agggggaatg cgagggggac tgacaggctg gggacacggg tggggcacag agaggaggcc   2155

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agttttatga tgtacagatg gagagagagg cagagagaga gagatccaca gaagtccatg   3415

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tctgcccca ggaccc ccg gaa caa aca caa gtt ccg cct gca tag cta cag   7367
                 Pro Glu Gln Thr Gln Val Pro Pro Ala     Leu Gln
                              160                 165

cag ccc cac ctt ctg cga cca ctg tgg ctc cct cct cta cgg gct tgt      7415
Gln Pro His Leu Leu Arg Pro Leu Trp Leu Pro Pro Leu Arg Ala Cys
        170                 175                 180

gca cca ggg cat gaa atg ctc ctg tga gt  gacctgggcc ttgccagggc        7464
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Ala Pro Gly His Glu Met Leu Leu     Val
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aga tga acg tgc acc ggc gct gtg tgc gta gcg tgc cct ccc tgt gcg    7628
Arg     Thr Cys Thr Gly Ala Val Cys Val Ala Cys Pro Pro Cys Ala
            195                 200                 205

gtg tgg acc aca ccg agc gcc gcg ggc gcc tgc agc tgg aga tcc ggg    7676
Val Trp Thr Thr Pro Ser Ala Ala Gly Ala Cys Ser Trp Arg Ser Gly
        210                 215                 220

ctc cca cag cag atg aga tcc acg taa ctg gtg agg ccccgccccc         7722
Leu Pro Gln Gln Met Arg Ser Thr     Leu Val Arg
    225                 230

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                            Glu Ala Arg Asn Leu Ile Pro Met Asp
                            235                 240

ccc aat ggt ctc tct gat ccc tat gtg aaa ctg aag ctc atc cca gac     9442
Pro Asn Gly Leu Ser Asp Pro Tyr Val Lys Leu Lys Leu Ile Pro Asp
    245                 250                 255

cct cgg aac ctg acg aaa cag aag acc cga acg gtg aaa gcc acg cta     9490
Pro Arg Asn Leu Thr Lys Gln Lys Thr Arg Thr Val Lys Ala Thr Leu
260                 265                 270                 275

aac cct gtg tgg aat gag acc ttt gtg ttg tga gt  ctggggtgca          9535
Asn Pro Val Trp Asn Glu Thr Phe Val Leu     Val
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        Leu Lys Pro Gly Asp Val Glu Arg Arg Leu Ser Val Glu Val
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Trp Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe Met Gly Ala Met Ser
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Phe Gly Val Ser Glu Leu Leu Lys Ala Pro Val Asp Gly Trp
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Leu Gln Pro Pro Pro Glu Val     Gly Thr
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              Ala Gly Ala Asp Gly Pro Leu Phe Leu Ser His Pro Leu
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Pro Phe Pro     Ser His Arg Pro Gln Ala Leu Leu Leu Arg Gly Glu
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Ser Arg Thr Pro Ala His Leu Arg Leu Gln Leu Pro His Gly Ser Arg
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Lys Arg Gln Phe Trp Glu
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Gly     Cys Trp Pro Ser Ala Gly Ala Leu Met Ser Ser Thr Pro Ser
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Arg Ser     Lys Arg Thr     Ser Ser Arg Thr Thr Met Trp Thr Ala
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cgc tgg tgg aga aac gtg tgc tgg cgc tgg ggg gcc ggg gtc ctg gcg    16270
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Cys Gly Arg Ser Gly Glu Asn Phe Asp Lys Phe Phe Thr Arg Ala Ala
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Pro Ala Leu Thr Pro Pro Asp Arg Leu Val Leu Ala Ser Ile Asp Gln
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Ala Asp Phe Gln Gly Phe Thr Tyr Val Asn Pro Asp Phe Val His Pro
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Asp Ala Arg Ser Pro Thr Ser Pro Val Pro Val Pro Val Met     Ser
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cac ccg ccg cca cta ggt gtc ccc aac gtc ccc tcc gcc gtg ccg gcg    24635
His Pro Pro Pro Leu Gly Val Pro Asn Val Pro Ser Ala Val Pro Ala
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Ala Ala Pro Leu His Pro Gln Leu His His Pro Leu Ser His Ser Arg
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Val Pro Cys Pro Ser Pro Ala His Leu Gly Ile Ser Leu Trp Leu Leu
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gaa agg cag gat cct ggt ccc tgc tac gtt tct ggg gcc atg gct ggt       192
Glu Arg Gln Asp Pro Gly Pro Cys Tyr Val Ser Gly Ala Met Ala Gly
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Leu Gly Pro Gly Val Gly Asp Ser Glu Gly Gly Pro Arg Pro Leu Phe
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Cys Arg Lys Gly Ala Leu Arg Gln Lys Val Val His Glu Val Lys Ser
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cac aag ttc acc gct cgc ttc ttc aag cag ccc acc ttc tgc agc cac       336
His Lys Phe Thr Ala Arg Phe Phe Lys Gln Pro Thr Phe Cys Ser His
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Arg     Glu Leu Gly Trp Phe Ile Asp Asp Ala Thr Asn Leu     Pro
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Ser Ser Val Gln Ala Leu Gly Arg Ala Pro Arg Arg Thr     Val Leu
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Gly Pro Glu Gln Thr Gln Val Pro Pro Ala     Leu Gln Gln Pro His
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Gln Cys Ala Gly Gly Arg Cys     Gln Leu Gln Pro Pro Pro Glu Val
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cga ccc caa gcg ctg ctt ctt cgg ggc gag tcc agg acg cct gca cat      1248
Arg Pro Gln Ala Leu Leu Leu Arg Gly Glu Ser Arg Thr Pro Ala His
                390                 395                 400

ctc cga ctt cag ctt cct cat ggt tct agg aaa agg cag ttt tgg gaa g    1297
Leu Arg Leu Gln Leu Pro His Gly Ser Arg Lys Arg Gln Phe Trp Glu
            405                 410                 415

gg  tga tgc tgg ccg agc gca ggg gct ctg atg agc tct acg cca tca      1344
Gly     Cys Trp Pro Ser Ala Gly Ala Leu Met Ser Ser Thr Pro Ser
            420                 425                 430

aga tct tga aaa agg acg tga tcg tcc agg acg acg atg tgg act gca      1392
Arg Ser     Lys Arg Thr     Ser Ser Arg Thr Thr Met Trp Thr Ala
            435                     440                 445

cgc tgg tgg aga aac gtg tgc tgg cgc tgg ggg gcc ggg gtc ctg gcg      1440
Arg Trp Trp Arg Asn Val Cys Trp Arg Trp Gly Ala Gly Val Leu Ala
            450                 455                 460

gcc ggc ccc act tcc tca ccc agc tcc act cca cct tcc aga ccc cg  g    1488
Ala Gly Pro Thr Ser Ser Pro Ser Ser Thr Pro Pro Ser Arg Pro Arg
        465                 470                 475

acc gcc tgt att tcg tga tgg agt acg tca ccg ggg gag act tga tgt      1536
Thr Ala Cys Ile Ser     Trp Ser Thr Ser Pro Gly Glu Thr     Cys
    480                     485                 490

acc aca ttc aac agc tgg gca agt tta agg agc ccc atg cag cg   g ttc   1584
Thr Thr Phe Asn Ser Trp Ala Ser Leu Arg Ser Pro Met Gln Arg    Phe
        495                 500                 505

tac gcg gca gaa atc gct atc ggc ctc ttc ttc ctt cac aat cag ggc      1632
Tyr Ala Ala Glu Ile Ala Ile Gly Leu Phe Phe Leu His Asn Gln Gly
    510                 515                 520

atc atc tac agg gga cct gaa gct gga caa tgt gat gct gga tgc tga      1680
Ile Ile Tyr Arg Gly Pro Glu Ala Gly Gln Cys Asp Ala Gly Cys
525                 530                 535

ggg aca cat caa gat cac tga ctt tgg cat gtg taa gga gaa cgt ctt      1728
Gly Thr His Gln Asp His     Leu Trp His Val     Gly Glu Arg Leu
540                 545                         550

ccc cgg gac gac aac ccg cac ctt ctg cgg gac ccc gga cta cat agc      1776
Pro Arg Asp Asp Asn Pro His Leu Leu Arg Asp Pro Gly Leu His Ser
    555                 560                 565

ccc gga gg  a tca ttg cct acc agc cct atg gga agt ctg tcg att ggt    1824
Pro Gly Gly   Ser Leu Pro Thr Ser Pro Met Gly Ser Leu Ser Ile Gly
570                   575                 580                 585

ggt cct ttg gag ttc tgc tgt atg aga tgt tgg cag gac agg cct ccc      1872
Gly Pro Leu Glu Phe Cys Cys Met Arg Cys Trp Gln Asp Arg Pro Pro
                590                 595                 600

ttc gat ggg gag gac gag gag gag ctg ttt cag gcc atc atg gaa caa      1920
Phe Asp Gly Glu Asp Glu Glu Glu Leu Phe Gln Ala Ile Met Glu Gln
            605                 610                 615

act gtc acc tac ccc aag tcg ctt tcc cgg gaa gcc gtg gcc atc tgc      1968
Thr Val Thr Tyr Pro Lys Ser Leu Ser Arg Glu Ala Val Ala Ile Cys
        620                 625                 630

aag ggg g gt  tcc tga cca agc acc cag gga agc gcc tgg gct cag ggc    2016
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Lys Gly   Gly Ser      Pro Ser Thr Gln Gly Ser Ala Trp Ala Gln Gly
    635                        640                 645

ctg atg ggg aac cta cca tcc gtg cac atg gct ttt tcc gct gga ttg      2064
Leu Met Gly Asn Leu Pro Ser Val His Met Ala Phe Ser Ala Gly Leu
    650                 655                 660

act ggg agc ggc tgg aac gat tgg aga tcc cgc ctc ctt tca gac ccc      2112
Thr Gly Ser Gly Trp Asn Asp Trp Arg Ser Arg Leu Leu Ser Asp Pro
665                 670                 675                 680

gcc cg  g tgt ggc cgc agc ggc gag aac ttt gac aag ttc ttc acg cgg    2160
Ala Arg   Cys Gly Arg Ser Gly Glu Asn Phe Asp Lys Phe Phe Thr Arg
                  685                 690                 695

gcg gcg cca gcg ctg acc cct cca gac cgc cta gtc ctg gcc agc atc      2208
Ala Ala Pro Ala Leu Thr Pro Pro Asp Arg Leu Val Leu Ala Ser Ile
            700                 705                 710

gac cag gcc gat ttc cag ggc ttc acc tac gtg aac ccc gac ttc gtg      2256
Asp Gln Ala Asp Phe Gln Gly Phe Thr Tyr Val Asn Pro Asp Phe Val
        715                 720                 725

cac ccg gat gcc cgc agc ccc acc agc cca gtg cct gtg ccc gtc atg      2304
His Pro Asp Ala Arg Ser Pro Thr Ser Pro Val Pro Val Pro Val Met
    730                 735                 740

taa tct cac ccg ccg cca cta ggt gtc ccc aac gtc ccc tcc gcc gtg      2352
    Ser His Pro Pro Pro Leu Gly Val Pro Asn Val Pro Ser Ala Val
    745                 750                 755

ccg gcg gca gcc cca ctt cac ccc caa ctt cac cac ccc ctg tcc cat      2400
Pro Ala Ala Ala Pro Leu His Pro Gln Leu His His Pro Leu Ser His
760                 765                 770                 775

tct aga tcc tgc acc cca gca ttc cag ctc tgc ccc cgc ggg ttc tag      2448
Ser Arg Ser Cys Thr Pro Ala Phe Gln Leu Cys Pro Arg Gly Phe
                780                 785                 790

acg ccc ctc cca agc gtt cct ggc ctt ctg aac tcc ata cag cct cta      2496
Thr Pro Leu Pro Ser Val Pro Gly Leu Leu Asn Ser Ile Gln Pro Leu
                795                 800                 805

cag ccg tcc cgc gtt caa gac ttg agc g                                2524
Gln Pro Ser Arg Val Gln Asp Leu Ser
            810                 815


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